

SEQUENCE LISTING

<110> Klinikum der Universitaet Muenchen Grosshadern-Innenstadt
 <120> Leptin antagonist and method for the quantitative measurement of leptin
 <130> LM01P002WO
 <150> DE 103 53 953.4
 <151> 2003-11-17
 <160> 8
 <170> PatentIn version 3.1
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 20 25 30
 Lys Phe Met Ser Thr Ser Ile Gly Asp Arg Val Asn Ile Thr Cys Lys
 35 40 45
 Ala Thr Gln Asn Val Arg Thr Ala Val Thr Trp Tyr Gln Gln Lys Pro
 50 55 60
 Gly Gln Ser Pro Gln Ala Leu Ile Phe Leu Ala Ser Asn Arg His Thr
 65 70 75 80
 Gly Val Pro Ala Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95
 Leu Thr Ile Asn Asn Val Lys Ser Glu Asp Leu Ala Asp Tyr Phe Cys
 100 105 110
 Leu Gln His Trp Asn Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu
 115 120 125
 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
 130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
 145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
 165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
 180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
 195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
 210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys Xaa Xaa
 225 230 235 240

Ser Arg Val Lys Arg Xaa Gln Ser Xaa Gly Gly Pro Gly Thr Pro Ile
 245 250 255

Arg Pro Ile Gly Xaa Pro Tyr Tyr Asn Ser Leu Gly Gly Gly Phe Gln
 260 265 270

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 <212> DNA
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 Xaa His Asn Pro Ile Pro Met Pro Thr Ala Ala Ala Gly Leu Leu
 1 5 10 15
 tta ctc gct gcc caa cca gcc atg gcc gag ctc gtg atg acc cag tct 95
 Leu Leu Ala Ala Gln Pro Ala Met Ala Glu Leu Val Met Thr Gln Ser
 20 25 30
 cca aaa ttc atg tcc aca tca ata gga gac agg gtc aat atc acc tgc 143
 Pro Lys Phe Met Ser Thr Ser Ile Gly Asp Arg Val Asn Ile Thr Cys
 35 40 45

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aag gcc act cag aat gtt cgt act gct gtt acc tgg tat caa cag aaa Lys Ala Thr Gln Asn Val Arg Thr Ala Val Thr Trp Tyr Gln Gln Lys 50 55 60	191
cca ggg cag tct cct caa gca ctg att ttc ttg gca tcc aac cgg cac Pro Gly Gln Ser Pro Gln Ala Leu Ile Phe Leu Ala Ser Asn Arg His 65 70 75	239
act ggt gtc cct gct cga ttc aca ggc agt gga tct ggg aca gat ttc Thr Gly Val Pro Ala Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe 80 85 90 95	287
act ctc acc att aac aat gtg aaa tct gaa gac ctg gca gat tat ttc Thr Leu Thr Ile Asn Asn Val Lys Ser Glu Asp Leu Ala Asp Tyr Phe 100 105 110	335
tgt cta caa cat tgg aat tat cct ctc acg ttc ggc tcg ggg aca aag Cys Leu Gln His Trp Asn Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys 115 120 125	383
ttg gaa ata aaa cgg gct gat gct gca cca act gta tcc atc ttc cca Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro 130 135 140	431
cca tcc agt gag cag tta aca tct gga ggt gcc tca gtc gtg tgc ttc Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe 145 150 155	479
ttg aac aac ttc tac ccc aaa gac atc aat gtc aag tgg aag att gat Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp 160 165 170 175	527
ggc agt gaa cga caa aat ggc gtc ctg aac agt tgg act gat cag gac Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp 180 185 190	575
agc aaa gac agc acc tac agc atg agc agc acc ctc acg ttg acc aag Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys 195 200 205	623
gac gag tat gaa cga cat aac agc tat acc tgt gag gcc act cac aag Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys 210 215 220	671
aca tca act tca ccc att gtc aag agc ttc aac agg gga gag tgt tag Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys 225 230 235	719
taa tct aga gtt aag cgg ccg caa tcg agg ggg ggc ccg gta ccc caa Ser Arg Val Lys Arg Pro Gln Ser Arg Gly Gly Pro Val Pro Gln 240 245 250	767
ttc gcc cta tag ggg ngc cgt att aca att cac tgg gcg gcg gtt ttc Phe Ala Leu Gly Xaa Arg Ile Thr Ile His Trp Ala Ala Val Phe 255 260 265	815
aan Xaa	818

<210> 3

<211> 292

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Val Ile Met Lys Tyr Leu Xaa Ala Tyr Gly Pro Ala Ala Gly Leu Leu
 20 25 30

Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Leu Glu Ser
 35 40 45

Gly Pro Gly Leu Val Ala Pro Ser Glu Ser Leu Ser Ile Thr Cys Thr
 50 55 60

Ile Ser Gly Phe Ser Leu Thr Asp Asp Gly Val Ser Trp Ile Arg Gln
 65 70 75 80

Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Gly Gly
 85 90 95

Ser Thr Tyr Phe Asn Ser Leu Phe Lys Ser Arg Leu Ser Ile Thr Arg
 100 105 110

Asp Asn Ser Lys Ser Gln Val Phe Leu Glu Met Asp Ser Leu Gln Thr
 115 120 125

Asp Asp Thr Ala Met Tyr Tyr Cys Ala Lys His Asp Gly His Glu Thr
 130 135 140

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Lys
 145 150 155 160

Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
 165 170 175

Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
 180 185 190

Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
 195 200 205

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His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
 210 215 220

Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
 225 230 235 240

Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
 245 250 255

Pro Arg Asp Cys Thr Ser His His His His His His Xaa Ala Ser Leu
 260 265 270

Val Val Ala Val Ala Leu His Ser Phe Val Xaa Ile Lys Ala Asn Arg
 275 280 285

Arg Pro Ala Xaa
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<210> 4
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 <212> DNA
 <213> Mus musculus

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 Leu Ala Xaa Arg Gly Gly Gly Arg Lys Ile Xaa Phe Xaa Arg Glu Thr
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 gtc ata atg aaa tac ctt ttn gcc tac ggg cca gcc gct gga ttg tta 96
 Val Ile Met Lys Tyr Leu Xaa Ala Tyr Gly Pro Ala Ala Gly Leu Leu
 20 25 30
 tta ctc gct gcc caa cca gcc atg gcc cag gtg aaa ctg ctc gag tca 144
 Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Leu Glu Ser
 35 40 45
 gga cct ggc ctg gtg gcg ccc tca gag agc ctg tcc atc aca tgc act 192
 Gly Pro Gly Leu Val Ala Pro Ser Glu Ser Leu Ser Ile Thr Cys Thr
 50 55 60
 atc tca ggg ttc tca tta acc gac gat ggt gta agc tgg att cgg cag 240
 Ile Ser Gly Phe Ser Leu Thr Asp Asp Gly Val Ser Trp Ile Arg Gln
 65 70 75 80
 cct cca gga aag ggt ctg gag tgg ctg gga gta ata tgg ggt ggt gga 288

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Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Gly	Gly	Gly	
				85					90					95		
agc	aca	tac	ttt	aat	tca	ctt	ttc	aaa	tcc	aga	ctg	agc	atc	acc	agg	336
Ser	Thr	Tyr	Phe	Asn	Ser	Leu	Phe	Lys	Ser	Arg	Leu	Ser	Ile	Thr	Arg	
			100					105					110			
gac	aac	tct	aag	agc	caa	gtt	ttc	tta	gaa	atg	gac	agt	cta	caa	act	384
Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Glu	Met	Asp	Ser	Leu	Gln	Thr	
		115					120					125				
gat	gac	aca	gcc	atg	tac	tac	tgc	gcc	aaa	cat	gac	gga	cac	gag	act	432
Asp	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Lys	His	Asp	Gly	His	Glu	Thr	
		130				135					140					
atg	gac	tat	tgg	ggt	caa	gga	acc	tca	gtc	acc	gtc	tcc	tca	tcc	aaa	480
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ser	Lys	
					150					155					160	
acg	aca	ccc	cca	tct	gtc	tat	cca	ctg	gcc	cct	gga	tct	gct	gcc	caa	528
Thr	Thr	Pro	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	
				165					170					175		
act	aac	tcc	atg	gtg	acc	ctg	gga	tgc	ctg	gtc	aag	ggc	tat	ttc	cct	576
Thr	Asn	Ser	Met	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	
			180					185					190			
gag	cca	gtg	aca	gtg	acc	tgg	aac	tct	gga	tcc	ctg	tcc	agc	ggg	gtg	624
Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	
		195					200					205				
cac	acc	ttc	cca	gct	gtc	ctg	cag	tct	gac	ctc	tac	act	ctg	agc	agc	672
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	
		210				215					220					
tca	gtg	act	gtc	ccc	tcc	agc	acc	tgg	ccc	agc	gag	acc	gtc	acc	tgc	720
Ser	Val	Thr	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	
					230					235					240	
aac	gtt	gcc	cac	ccg	gcc	agc	agc	acc	aag	gtg	gac	aag	aaa	att	gtg	768
Asn	Val	Ala	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	
				245					250					255		
ccc	agg	gat	tgt	act	agt	cat	cat	cat	cat	cat	cat	taa	gct	agc	cta	816
Pro	Arg	Asp	Cys	Thr	Ser	His	His	His	His	His	His		Ala	Ser	Leu	
			260					265						270		
gtg	gtg	gcg	gtg	gct	ctc	cat	tcg	ttt	gtg	ang	ata	aag	gcc	aat	cgn	864
Val	Val	Ala	Val	Ala	Leu	His	Ser	Phe	Val	Xaa	Ile	Lys	Ala	Asn	Arg	
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aga	cct	gcn	cna													876
Arg	Pro	Ala	Xaa													
			290													

<210> 5
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<223> n = a, t, g, c, any or other

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cag gag tca gga act gaa gtg gta aag cct ggg gct tca gtg aag ttg      103
Gln Glu Ser Gly Thr Glu Val Val Lys Pro Gly Ala Ser Val Lys Leu
                               10                               15                               20

tcc tgc aag gct tct ggc tac atc ttc aca agt tat gat ata gac tgg      151
Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Ser Tyr Asp Ile Asp Trp
                               25                               30                               35

gtg agg cag acg cct gaa cag gga ctt gag tgg att gga tgg att ttt      199
Val Arg Gln Thr Pro Glu Gln Gly Leu Glu Trp Ile Gly Trp Ile Phe
                               40                               45                               50

cct gga gag ggg agt act gaa tac aat gag aag ttc aag ggc agg gcc      247
Pro Gly Glu Gly Ser Thr Glu Tyr Asn Glu Lys Phe Lys Gly Arg Ala
55                               60                               65                               70

aca ctg agt gta gac aag tcc tcc agc aca gcc tat atg gag ctc act      295
Thr Leu Ser Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Thr
                               75                               80                               85

agg ctg aca tct gag gac tct gct gtc tat ttc tgt gct aga ggg gac      343
Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Gly Asp
                               90                               95                               100

tac tat agg cgc tac ttt gac ttg tgg ggc caa ggg acc acg gtc acc      391
Tyr Tyr Arg Arg Tyr Phe Asp Leu Trp Gly Gln Gly Thr Thr Val Thr
                               105                               110                               115

gtc tcc tca tgt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc      439
Val Ser Ser Cys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                               120                               125                               130

gga tct gac att gag ctc acc cag tct cca gca atc atg tct gca tct      487
Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
135                               140                               145                               150

cca ggg gag agg gtc acc atg acc tgc agt gcc agc tca agt ata cgt      535
Pro Gly Glu Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Ile Arg
                               155                               160                               165

tac ata tat tgg tac caa cag aag cct gga tcc tcc ccc aga ctc ctg      583
Tyr Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Arg Leu Leu
                               170                               175                               180

att tat gac aca tcc aac gtg gct cct gga gtc cct ttt cgc ttc agt      631
Ile Tyr Asp Thr Ser Asn Val Ala Pro Gly Val Pro Phe Arg Phe Ser
                               185                               190                               195

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ggc agt ggg tct ggg acc tct tat tct ctc aca atc aac cga atg gag 679
 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Asn Arg Met Glu
 200 205 210

gct gag gat gct gcc act tat tac tgc cag gag tgg agt ggt tat cct 727
 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Glu Trp Ser Gly Tyr Pro
 215 220 225 230

ctc acg ttc ggc tcg ggc acc aag cgg gaa atc aaa cgg gcg gcc gca 775
 Leu Thr Phe Gly Ser Gly Thr Lys Arg Glu Ile Lys Arg Ala Ala Ala
 235 240 245

ggt gcg ccg gtg ccg tat ccg gat ccg ctg gaa ccg cgt gccgcataga 824
 Gly Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg
 250 255

ctgttgaa 832

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 20 25 30

Ser Tyr Asp Ile Asp Trp Val Arg Gln Thr Pro Glu Gln Gly Leu Glu
 35 40 45

Trp Ile Gly Trp Ile Phe Pro Gly Glu Gly Ser Thr Glu Tyr Asn Glu
 50 55 60

Lys Phe Lys Gly Arg Ala Thr Leu Ser Val Asp Lys Ser Ser Ser Thr
 65 70 75 80

Ala Tyr Met Glu Leu Thr Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr
 85 90 95

Phe Cys Ala Arg Gly Asp Tyr Tyr Arg Arg Tyr Phe Asp Leu Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Cys Gly Gly Gly Ser Gly Gly
 115 120 125

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Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro
 130 135 140

Ala Ile Met Ser Ala Ser Pro Gly Glu Arg Val Thr Met Thr Cys Ser
 145 150 155 160

Ala Ser Ser Ser Ile Arg Tyr Ile Tyr Trp Tyr Gln Gln Lys Pro Gly
 165 170 175

Ser Ser Pro Arg Leu Leu Ile Tyr Asp Thr Ser Asn Val Ala Pro Gly
 180 185 190

Val Pro Phe Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
 195 200 205

Thr Ile Asn Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 210 215 220

Glu Trp Ser Gly Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Arg Glu
 225 230 235 240

Ile Lys Arg Ala Ala Ala Gly Ala Pro Val Pro Tyr Pro Asp Pro Leu
 245 250 255

Glu Pro Arg

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<212> DNA

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gtgtaagctg gattcggcag cctccaggaa agggctctgga gtggctggga gtaatatggg	180
gtggtggaag cacatacttt aattcacttt tcaaattccag actgagcatc accagggaca	240
actctaagag ccaagttttc ttagaaatgg acagtctaca aactgatgac acagccatgt	300
actactgctc caaacatgac ggacacgaga ctatggacta ttgggggtcaa ggaacctcag	360
tcaccgtctc ctcatccaaa acgacacccc catctgtcta tccactggcc cctggatctg	420
ctgcccacaaac taactccatg gtgaccctgg gatgcctggt caagggctat ttccctgagc	480

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cagtgcacagt gacctggaac tctggatccc tgtccagcgg tgtgcacacc ttcccagctg      540
tcctgcagtc tgacctctac actctgagca gctcagtgac tgtcccctcc agcacctggc      600
ccagcgagac cgtcacctgc aacgttgccc acccggccag cagcaccaag gtggacaaga      660
aaattgtgcc cagggattgt actagtgggtg gcggaggtag tggtaggcgga ggtagcgggtg      720
gcggagggttc tggtaggcgga ggttcogaat tcctcgaggt gcccatccaa aaagtccaag      780
atgacaccaa aaccctcatc aagacaattg tcaccaggat caatgacatt tcacacacgc      840
agtcagtctc ctccaaacag aaagtcaccg gtttggaactt cattcctggg ctccacccca      900
tcctgacctt atccaagatg gaccagacac tggcagtcta ccaacagatc ctcaccagta      960
tgccttccag aaacgtgatc caaatatcca acgacctgga gaacctccgg gatcttcttc     1020
acgtgctggc cttctctaag agctgccact tgccctgggc cagtggcctg gagaccttgg     1080
acagcctggg ggggtgtcctg gaagcttcag gctactccac agaggtaggtg gccctgagca     1140
ggctgcaggg gtctctgcag gacatgctgt ggcagctgga cctcagccct gggtagcacta     1200
gtcatcatca tcatcatcat taagctagcc tagtggtggc ggtggctctc ca              1252

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<210> 8

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Met Ala Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Ala Pro
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Ser Glu Ser Leu Ser Ile Thr Cys Thr Ile Ser Gly Phe Ser Leu Thr
          20              25             30

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Asp Asp Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
          35              40             45

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Trp Leu Gly Val Ile Trp Gly Gly Gly Ser Thr Tyr Phe Asn Ser Leu
          50              55             60

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Phe Lys Ser Arg Leu Ser Ile Thr Arg Asp Asn Ser Lys Ser Gln Val
65              70              75             80

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Phe Leu Glu Met Asp Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr
          85              90             95

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Cys Ala Lys His Asp Gly His Glu Thr Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Ser Val Thr Val Ser Ser Ser Lys Thr Thr Pro Pro Ser Val Tyr
 115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
 130 135 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
 145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
 180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Thr Ser Gly
 210 215 220

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 225 230 235 240

Gly Gly Ser Glu Phe Leu Glu Val Pro Ile Gln Lys Val Gln Asp Asp
 245 250 255

Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser
 260 265 270

His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe
 275 280 285

Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr
 290 295 300

Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val
 305 310 315 320

Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val
 325 330 335

Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu

340

345

350

Thr Leu Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr
355 360 365

Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu
370 375 380

Trp Gln Leu Asp Leu Ser Pro Gly Cys Thr Ser His His His His His
385 390 395 400

His